

In the Specification

Please amend the paragraph beginning at page 17, line 6, as follows:

In general homologs and alleles typically will share at least 40% nucleotide identity and/or at least 50% amino acid identity to the sequences of breast cancer associated antigen nucleic acid and polypeptides, respectively, in some instances will share at least 50% nucleotide identity and/or at least 65% amino acid identity and in still other instances will share at least 60% nucleotide identity and/or at least 75% amino acid identity. The homology can be calculated using various, publicly available software tools developed by the National Center for Biotechnology Information NCBI (NCBI, Bethesda, Maryland) that can be obtained through the internet (~~ftp://ncbi.nlm.nih.gov/pub/~~). Exemplary tools include the BLAST system available at the NCBI website ~~http://www.ncbi.nlm.nih.gov~~. Pairwise and ClustalW alignments (BLOSUM30 matrix setting) as well as Kyte-Doolittle hydropathic analysis can be obtained using the ~~MaeVetor~~ MacVector sequence analysis software (Oxford Molecular Group). Watson-Crick complements of the foregoing nucleic acids also are embraced by the invention.

Please amend the paragraph beginning at page 84, line 17, as follows:

One also can search for class I and class II motifs using computer algorithms. For example, computer programs for predicting potential CTL epitopes based on known class I motifs has been described (*see, e.g.,* Parker et al, *J. Immunol.* 152:163, 1994; D'Amaro et al., *Human Immunol.* 43:13-18, 1995; Drijfhout et al., *Human Immunol.* 43:1-12, 1995). HLA binding predictions can conveniently be made using an algorithm available via the Internet on the National Institutes of Health ~~World Wide Web~~ website at URL ~~http://bimas.dert.nih.gov~~. Methods for determining HLA class II peptides and making substitutions thereto are also known (e.g. Strominger and Wucherpfennig (PCT/US96/03182)).